

T.0400  
(1) GENERAL INFORMATION:

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(i) APPLICANT: Glimcher, Laurie H.  
Hodge, Martin R.

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(ii) TITLE OF INVENTION: NF-AT-INTERACTING PROTEIN NIP45 AND METHODS  
OF USE THEREFOR

(iii) NUMBER OF SEQUENCES: 2

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD  
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(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109-1875

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Giulio A. DeConti, Jr.  
(B) REGISTRATION NUMBER: 31,503  
(C) REFERENCE/DOCKET NUMBER: HUI-026

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1946 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 13..1248

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5	ACAGTGTGGG AG ATG GCG GAA CCA CTG AGG GGA CGT GGT CCG AGG TCC	48
	Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser	
	1 5 10	
10	CGC GGT GGC CGA GGC GCT CGG AGA GCC CGA GGC GCC CGT GGC CGG TGT	96
	Arg Gly Gly Arg Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys	
	15 20 25	
15	CCT CGC GCC CGG CAG TCT CCG GCT AGG CTC ATT CCA GAC ACC GTG CTT	144
	Pro Arg Ala Arg Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu	
	30 35 40	
20	GTG GAC TTG GTC AGT GAC AGC GAC GAA GAG GTC TTG GAA GTC GCA GAC	192
	Val Asp Leu Val Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp	
	45 50 55 60	
25	CCA GTA GAG GTG CCG GTC GCC CGC CTC CCC GCG CCG GCT AAA CCT GAG	240
	Pro Val Glu Val Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu	
	65 70 75	
30	CAG GAC AGC GAC AGT GAC AGT GAA GGG GCG GCC GAG GGG CCT GCG GGA	288
	Gln Asp Ser Asp Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly	
	80 85 90	
35	GCC CCG CGT ACA TTG GTG CGA CGG CGG CGG CGG CGG CTG CTG GAT CCC	336
	Ala Pro Arg Thr Leu Val Arg Arg Arg Arg Arg Arg Leu Leu Asp Pro	
	95 100 105	
40	GGA GAG GCG CCG GTG GTC CCA GTG TAC TCC GGG AAG GTA CAG AGC AGC	384
	Gly Glu Ala Pro Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser	
	110 115 120	
45	CTC AAC CTC ATT CCA GAT AAT TCA TCC CTC TTG AAA CTG TGC CCT TCA	432
	Leu Asn Leu Ile Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser	
	125 130 135 140	
50	GAG CCT GAA GAT GAG GCA GAT CTG ACA AAT TCT GGC AGT TCT CCC TCT	480
	Glu Pro Glu Asp Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser	
	145 150 155	
55	GAG GAT GAT GCC CTG CCT TCA GGT TCT CCC TGG AGA AAG AAG CTC AGA	528
	Glu Asp Asp Ala Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg	
	160 165 170	
60	AAG AAG TGT GAG AAA GAA GAA AAG AAA ATG GAA GAG TTT CCG GAC CAG	576
	Lys Lys Cys Glu Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln	
	175 180 185	
65	GAC ATC TCT CCT TTG CCC CAA CCT TCG TCA AGG AAC AAA AGC AGA AAG	624
	Asp Ile Ser Pro Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys	
	190 195 200	
70	CAT ACG GAG GCG CTC CAG AAG CTA AGG GAA GTG AAC AAG CGT CTC CAA	672
	His Thr Glu Ala Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln	
	205 210 215 220	

	GAT CTC CGC TCC TGC CTG AGC CCC AAG CAG CAC CAG AGT CCA GCC CTT	720
	Asp Leu Arg Ser Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu	
	225 230 235	
5	CAG AGC ACA GAT GAT GAG GTG GTC CTA GTG GAA GGG CCT GTC TTG CCA	768
	Gln Ser Thr Asp Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro	
	240 245 250	
10	CAG AGC TCT CGA CTC TTT ACA CTC AAG ATC CGG TGC CGG GCT GAC CTA	816
	Gln Ser Ser Arg Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu	
	255 260 265	
15	GTG AGA CTG CCT GTC AGG ATG TCG GAG CCC CTT CAG AAT GTG GTG GAT	864
	Val Arg Leu Pro Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp	
	270 275 280	
20	CAC ATG GCC AAT CAT CTT GGG GTG TCT CCA AAC AGG ATT CTT TTG CTT	912
	His Met Ala Asn His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu	
	285 290 295 300	
25	TTT GGA GAG AGT GAA CTG TCT CCT ACT GCC ACC CCT AGT ACC CTA AAG	960
	Phe Gly Glu Ser Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys	
	305 310 315	
30	CTT GGA GTG GCT GAC ATC ATT GAT TGT GTG GTG CTA GCA AGC TCT TCA	1008
	Leu Gly Val Ala Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser	
	320 325 330	
35	GAG GCC ACA GAG ACA TCC CAG GAG CTC CGG CTC CGG GTG CAG GGG AAG	1056
	Glu Ala Thr Glu Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys	
	335 340 345	
40	GAG AAA CAC CAG ATG TTG GAG ATC TCA CTG TCT CCT GAT TCT CCT CTT	1104
	Glu Lys His Gln Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu	
	350 355 360	
45	AAG GTT CTC ATG TCA CAC TAT GAG GAA GCC ATG GGA CTC TCT GGA CAC	1152
	Lys Val Leu Met Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His	
	365 370 375 380	
50	AAG CTC TCC TTC TTC TTT GAT GGG ACA AAG CTT TCA GGC AAG GAG CTG	1200
	Lys Leu Ser Phe Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu	
	385 390 395	
55	CCA GCT GAT CTG GGC CTG GAA TCC GGA GAT CTC ATC GAA GTC TGG GGC	1248
	Pro Ala Asp Leu Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly	
	400 405 410	
60	TGAAGCTCTC ACCCTGTTTCG GACGCAAAGC CAAGACATGG AGACAATAGC TCCCAATTTT	1308
65	ATTATTGTGA TTTTTCGCCC CATAAGGGCT AACAGAAACT GAATTAGAAC TTGTTTACTT	1368
70	ATTTATTTCT GGTGCTGGGG ATTGAACCCC AGACTATGCA CATGCTAAGG ATGTATGAAG	1428
75	TGGAGGCAAA ACCAAGGCAT TACCTTTAGC CAGCCTCTAG TAGACTGTAG TGTCAAGCAA	1488
80	GTGGCTACTT GGTAGTTGTG TGGCTCTGTG TATGTTTGTG CTGTATTGG CAGCCCCTGG	1548

GGCACATAGA AGGGACCTTG GCTTCCCTAC CATTTACGT TCGCTGGTGC CCTTTCCTTC 1608  
 ATCAGATGAC TTCTGTGAAG CTGCCTATGT TGAGTGTGTT GAACTAAATG AGCTCTGCTT 1668  
 5 TGGGTGTCCA GGCCTGGGGT TTGTGCCGCA GTTGGAGCCA GCAGTGA CACTCTGACT 1728  
 TGGGACTGAG AATGCATTTT CTGGTGGAGA CACTCGGGTG CAGAAATATA ACAGAAGGTG 1788  
 10 ACATACATGC TGAAGCTGAG GACTAGGTCG AAAGTTAACG ACGTTGCATT TTCAGCCTTG 1848  
 GGTATCCTCT CTGCCTGCCA GGA CTCTAGC CAGTGTCTGG TACACACTTC TTGGCATGGA 1908  
 CACCTAGGTC GACGCGGGCG CGATTTCGGCC GACTCGAG 1946

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Glu Pro Leu Arg Gly Arg Gly Pro Arg Ser Arg Gly Gly Arg  
 1 5 10 15  
 30 Gly Ala Arg Arg Ala Arg Gly Ala Arg Gly Arg Cys Pro Arg Ala Arg  
 20 25 30  
 Gln Ser Pro Ala Arg Leu Ile Pro Asp Thr Val Leu Val Asp Leu Val  
 35 35 40 45  
 Ser Asp Ser Asp Glu Glu Val Leu Glu Val Ala Asp Pro Val Glu Val  
 50 55 60  
 40 Pro Val Ala Arg Leu Pro Ala Pro Ala Lys Pro Glu Gln Asp Ser Asp  
 65 70 75 80  
 Ser Asp Ser Glu Gly Ala Ala Glu Gly Pro Ala Gly Ala Pro Arg Thr  
 85 90 95  
 45 Leu Val Arg Arg Arg Arg Arg Arg Leu Leu Asp Pro Gly Glu Ala Pro  
 100 105 110  
 Val Val Pro Val Tyr Ser Gly Lys Val Gln Ser Ser Leu Asn Leu Ile  
 115 120 125  
 50 Pro Asp Asn Ser Ser Leu Leu Lys Leu Cys Pro Ser Glu Pro Glu Asp  
 130 135 140  
 Glu Ala Asp Leu Thr Asn Ser Gly Ser Ser Pro Ser Glu Asp Asp Ala  
 145 150 155 160  
 Leu Pro Ser Gly Ser Pro Trp Arg Lys Lys Leu Arg Lys Lys Cys Glu  
 165 170 175

Lys Glu Glu Lys Lys Met Glu Glu Phe Pro Asp Gln Asp Ile Ser Pro  
 180 185 190  
 5 Leu Pro Gln Pro Ser Ser Arg Asn Lys Ser Arg Lys His Thr Glu Ala  
 195 200 205  
 Leu Gln Lys Leu Arg Glu Val Asn Lys Arg Leu Gln Asp Leu Arg Ser  
 210 215 220  
 10 Cys Leu Ser Pro Lys Gln His Gln Ser Pro Ala Leu Gln Ser Thr Asp  
 225 230 235 240  
 Asp Glu Val Val Leu Val Glu Gly Pro Val Leu Pro Gln Ser Ser Arg  
 245 250 255  
 15 Leu Phe Thr Leu Lys Ile Arg Cys Arg Ala Asp Leu Val Arg Leu Pro  
 260 265 270  
 Val Arg Met Ser Glu Pro Leu Gln Asn Val Val Asp His Met Ala Asn  
 275 280 285  
 His Leu Gly Val Ser Pro Asn Arg Ile Leu Leu Leu Phe Gly Glu Ser  
 290 295 300  
 25 Glu Leu Ser Pro Thr Ala Thr Pro Ser Thr Leu Lys Leu Gly Val Ala  
 305 310 315 320  
 Asp Ile Ile Asp Cys Val Val Leu Ala Ser Ser Ser Glu Ala Thr Glu  
 325 330 335  
 30 Thr Ser Gln Glu Leu Arg Leu Arg Val Gln Gly Lys Glu Lys His Gln  
 340 345 350  
 Met Leu Glu Ile Ser Leu Ser Pro Asp Ser Pro Leu Lys Val Leu Met  
 355 360 365  
 Ser His Tyr Glu Glu Ala Met Gly Leu Ser Gly His Lys Leu Ser Phe  
 370 375 380  
 40 Phe Phe Asp Gly Thr Lys Leu Ser Gly Lys Glu Leu Pro Ala Asp Leu  
 385 390 395 400  
 Gly Leu Glu Ser Gly Asp Leu Ile Glu Val Trp Gly  
 405 410

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